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RAW SEQUENCE LISTING

DATE: 03/01/2002

PATENT APPLICATION: US/10/072,436

TIME: 11:01:01

Input Set : A:\1803.txt

Output Set: N:\CRF3\03012002\J072436.raw

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5 <110> APPLICANT: MARKAU, URSULA
7   EBENBICHLER, CHRISTINE
9   ACHHAMMER, GUNTAR
11  ANKENBAUER, WALTRAUD
15 <120> TITLE OF INVENTION: MODIFIED DNA-POLYMERASE FROM CARBOXYDOTHENUS
HYDROGENOFORMANS AND
16   ITS USE FOR COUPLED REVERSE TRANSCRIPTION AND POLYMERASE CHAIN REACTION
20 <130> FILE REFERENCE: 1803-332-999
C--> 23 <140> CURRENT APPLICATION NUMBER: US/10/072,436
C--> 23 <141> CURRENT FILING DATE: 2002-02-05
23 <150> PRIOR APPLICATION NUMBER: 09/204,208
25 <151> PRIOR FILING DATE: 1998-12-01
29 <150> PRIOR APPLICATION NUMBER: EP 97121151.1
31 <151> PRIOR FILING DATE: 1997-12-02
35 <160> NUMBER OF SEQ ID NOS: 12
39 <170> SOFTWARE: PatentIn version 3.0
43 <210> SEQ ID NO: 1
45 <211> LENGTH: 18
47 <212> TYPE: DNA
C--> 49 <213> ORGANISM: Artificial
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53 <223> OTHER INFORMATION: Description of artificial sequence: amplification primer
57 <220> FEATURE:
59 <221> NAME/KEY: misc_feature
61 <222> LOCATION: (3)..(3)
63 <223> OTHER INFORMATION: any nucleotide
67 <220> FEATURE:
69 <221> NAME/KEY: misc_feature
71 <222> LOCATION: (9)..(9)
73 <223> OTHER INFORMATION: any nucleotide
77 <400> SEQUENCE: 1
W--> 78 ccnaaaytnc araayath 18
81 <210> SEQ ID NO: 2
83 <211> LENGTH: 15
85 <212> TYPE: DNA
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89 <220> FEATURE:
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97 <221> NAME/KEY: misc_feature
99 <222> LOCATION: (10)..(10)
101 <223> OTHER INFORMATION: any nucleotide
105 <400> SEQUENCE: 2
W--> 106 ytcrtcrtgn acytg 15

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117 <220> FEATURE:
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127 <210> SEQ ID NO: 4
129 <211> LENGTH: 28
131 <212> TYPE: DNA
C--> 133 <213> ORGANISM: Artificial
135 <220> FEATURE:
137 <223> OTHER INFORMATION: Description of artificial sequence: amplification primer
141 <400> SEQUENCE: 4
142 gaagccttaa ttcaatctgg gaataatc 28
145 <210> SEQ ID NO: 5
147 <211> LENGTH: 36
149 <212> TYPE: DNA
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153 <220> FEATURE:
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167 <212> TYPE: DNA
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173 <223> OTHER INFORMATION: Description of artificial sequence: amplification primer
177 <400> SEQUENCE: 6
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185 <212> TYPE: DNA
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189 <220> FEATURE:
191 <223> OTHER INFORMATION: Description of artificial sequence: amplification primer
195 <400> SEQUENCE: 7
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203 <212> TYPE: DNA
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207 <220> FEATURE:
209 <223> OTHER INFORMATION: Description of artificial sequence: amplification primer
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214 cgggaatcca tggaaaagct tgccgaacac gaaaattta 39
217 <210> SEQ ID NO: 9

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227 <223> OTHER INFORMATION: Description of artificial sequence: amplification primer
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237 <211> LENGTH: 1824
239 <212> TYPE: DNA
241 <213> ORGANISM: Carboxydotherrmus hydrogenoformans
245 <220> FEATURE:
247 <221> NAME/KEY: CDS
249 <222> LOCATION: (1)..(1824)
253 <400> SEQUENCE: 10
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256 1 5 10 15
258 tta gct aca atc ctg cgg gaa ata ccg tta gaa atc tcc ctg gaa gat 96
259 Leu Ala Thr Ile Leu Arg Glu Ile Pro Leu Glu Ile Ser Leu Glu Asp
260 20 25 30
262 tta aaa gtt aaa gaa cct aat tat gaa gaa gtt gct aaa tta ttt ctt 144
263 Leu Lys Val Lys Glu Pro Asn Tyr Glu Glu Val Ala Lys Leu Phe Leu
264 35 40 45
266 cac ctt gag ttt aaa agc ttt tta aaa gaa ata gaa cca aaa ata aag 192
267 His Leu Glu Phe Lys Ser Phe Leu Lys Glu Ile Glu Pro Lys Ile Lys
268 50 55 60
270 aaa gaa tac cag gaa ggt aaa gat ttg gtg caa gtt gaa act gta gaa 240
271 Lys Glu Tyr Gln Glu Gly Lys Asp Leu Val Gln Val Glu Thr Val Glu
272 65 70 75 80
274 acg gaa gga cag att gca gta gtt ttt agt gat gga ttt tat gtt gat 288
275 Thr Glu Gly Gln Ile Ala Val Val Phe Ser Asp Gly Phe Tyr Val Asp
276 85 90 95
278 gac ggg gaa aaa aca aag ttt tac tct tta gac cgg ctg aat gaa ata 336
279 Asp Gly Glu Lys Thr Lys Phe Tyr Ser Leu Asp Arg Leu Asn Glu Ile
280 100 105 110
282 gag gaa ata ttt agg aat aaa aaa att att acc gac gat gcc aaa gga 384
283 Glu Glu Ile Phe Arg Asn Lys Lys Ile Ile Thr Asp Asp Ala Lys Gly
284 115 120 125
286 att tat cat gtc tgt tta gaa aaa ggt ctg act ttt ccc gaa gtt tgt 432
287 Ile Tyr His Val Cys Leu Glu Lys Gly Leu Thr Phe Pro Glu Val Cys
288 130 135 140
290 ttt gat gcg cgg att gca gct tat gtt tta aac ccg gcc gac caa aat 480
291 Phe Asp Ala Arg Ile Ala Ala Tyr Val Leu Asn Pro Ala Asp Gln Asn
292 145 150 155 160
294 ccc ggc ctc aag ggg ctt tat cta aag tat gac tta ccg gtg tat gaa 528
295 Pro Gly Leu Lys Gly Leu Tyr Leu Lys Tyr Asp Leu Pro Val Tyr Glu
296 165 170 175
298 gat gta tct tta aac att aga ggg ttg ttt tat tta aaa aaa gaa atg 576

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299	Asp	Val	Ser	Leu	Asn	Ile	Arg	Gly	Leu	Phe	Tyr	Leu	Lys	Lys	Glu	Met	
300				180					185				190				
302	atg	aga	aaa	atc	ttt	gag	cag	gag	caa	gaa	agg	tta	ttt	tat	gaa	ata	624
303	Met	Arg	Lys	Ile	Phe	Glu	Gln	Glu	Gln	Glu	Arg	Leu	Phe	Tyr	Glu	Ile	
304			195					200				205					
306	gaa	ctt	cct	tta	act	cca	gtt	ctt	gct	caa	atg	gag	cat	acc	ggc	att	672
307	Glu	Leu	Pro	Leu	Thr	Pro	Val	Leu	Ala	Gln	Met	Glu	His	Thr	Gly	Ile	
308		210					215					220					
310	cag	gtt	gac	cgg	gaa	gct	tta	aaa	gag	atg	tcg	tta	gag	ctg	gga	gag	720
311	Gln	Val	Asp	Arg	Glu	Ala	Leu	Lys	Glu	Met	Ser	Leu	Glu	Leu	Gly	Glu	
312	225				230				235						240		
314	caa	att	gaa	gag	tta	atc	cgg	gaa	att	tat	gtg	ctg	gcg	ggg	gaa	gag	768
315	Gln	Ile	Glu	Glu	Leu	Ile	Arg	Glu	Ile	Tyr	Val	Leu	Ala	Gly	Glu	Glu	
316				245					250					255			
318	ttt	aac	tta	aac	tcg	ccc	agg	cag	ctg	gga	gtt	att	ctt	ttt	gaa	aaa	816
319	Phe	Asn	Leu	Asn	Ser	Pro	Arg	Gln	Leu	Gly	Val	Ile	Leu	Phe	Glu	Lys	
320			260						265				270				
322	ctt	ggg	ctg	ccg	gta	att	aaa	aag	acc	aaa	acg	ggc	tac	tct	acc	gat	864
323	Leu	Gly	Leu	Pro	Val	Ile	Lys	Lys	Thr	Lys	Thr	Gly	Tyr	Ser	Thr	Asp	
324		275					280					285					
327	gcg	gag	gtt	ttg	gaa	gag	ctc	ttg	cct	ttc	cac	gaa	att	atc	ggc	aaa	912
328	Ala	Glu	Val	Leu	Glu	Glu	Leu	Leu	Pro	Phe	His	Glu	Ile	Ile	Gly	Lys	
329		290					295					300					
332	ata	ttg	aat	tac	cgg	cag	ctt	atg	aag	tta	aaa	tcc	act	tat	act	gac	960
333	Ile	Leu	Asn	Tyr	Arg	Gln	Leu	Met	Lys	Leu	Lys	Ser	Thr	Tyr	Thr	Asp	
334	305				310					315					320		
336	ggc	tta	atg	cct	tta	ata	aat	gag	cgt	acc	ggt	aaa	ctt	cac	act	act	1008
337	Gly	Leu	Met	Pro	Leu	Ile	Asn	Glu	Arg	Thr	Gly	Lys	Leu	His	Thr	Thr	
338				325					330					335			
340	ttt	aac	cag	acc	ggt	act	tta	acc	gga	cgc	ctg	gcg	tct	tcg	gag	ccc	1056
341	Phe	Asn	Gln	Thr	Gly	Thr	Leu	Thr	Gly	Arg	Leu	Ala	Ser	Ser	Glu	Pro	
342			340						345				350				
344	aat	ctc	caa	aat	att	ccc	atc	cgg	ttg	gaa	ctc	ggt	cgg	aaa	tta	cgc	1104
345	Asn	Leu	Gln	Asn	Ile	Pro	Ile	Arg	Leu	Glu	Leu	Gly	Arg	Lys	Leu	Arg	
346		355						360				365					
348	aag	atg	ttt	ata	cct	tca	ccg	ggg	tat	gat	tat	att	gtt	tcg	gcg	gat	1152
349	Lys	Met	Phe	Ile	Pro	Ser	Pro	Gly	Tyr	Asp	Tyr	Ile	Val	Ser	Ala	Asp	
350		370					375					380					
352	tat	tcc	cag	att	gaa	tta	agg	ctt	ctt	gcc	cat	ttt	tcc	gaa	gag	ccc	1200
353	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Leu	Leu	Ala	His	Phe	Ser	Glu	Glu	Pro	
354	385				390					395					400		
356	aag	ctt	att	gaa	gct	tac	caa	aaa	ggg	gag	gat	att	cac	cgg	aaa	acg	1248
357	Lys	Leu	Ile	Glu	Ala	Tyr	Gln	Lys	Gly	Glu	Asp	Ile	His	Arg	Lys	Thr	
358				405					410					415			
360	gcc	tcc	gag	gtg	ttc	ggt	gta	tct	ttg	gaa	gaa	gtt	act	ccc	gag	atg	1296
361	Ala	Ser	Glu	Val	Phe	Gly	Val	Ser	Leu	Glu	Glu	Val	Thr	Pro	Glu	Met	
362			420						425				430				
364	cgc	gct	cat	gcc	aag	tcg	gtg	aac	ttc	ggc	att	gtt	tat	ggc	att	agt	1344
365	Arg	Ala	His	Ala	Lys	Ser	Val	Asn	Phe	Gly	Ile	Val	Tyr	Gly	Ile	Ser	

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366          435          440          445
368 gat ttt ggt tta ggc aga gac tta aag att ccc cgg gag gtt gcc ggt      1392
369 Asp Phe Gly Leu Gly Arg Asp Leu Lys Ile Pro Arg Glu Val Ala Gly
370          450          455          460
372 aag tac att aaa aat tat ttt gcc aac tat ccc aaa gtg cgg gag tat      1440
373 Lys Tyr Ile Lys Asn Tyr Phe Ala Asn Tyr Pro Lys Val Arg Glu Tyr
374 465          470          475          480
376 ctc gat gaa ctt gtc cgt acg gca aga gaa aag gga tat gtg acc act      1488
377 Leu Asp Glu Leu Val Arg Thr Ala Arg Glu Lys Gly Tyr Val Thr Thr
378          485          490          495
380 tta ttt ggg cga aga cgc tat att cct gag cta tct tca aaa aac cgc      1536
381 Leu Phe Gly Arg Arg Arg Tyr Ile Pro Glu Leu Ser Ser Lys Asn Arg
382          500          505          510
384 acg gtt cag ggt ttt ggc gaa agg acg gcc atg aat act ccc ctt cag      1584
385 Thr Val Gln Gly Phe Gly Glu Arg Thr Ala Met Asn Thr Pro Leu Gln
386          515          520          525
388 ggc tcg gct gcc gat att att aag ctt gca atg att aat gta gaa aaa      1632
389 Gly Ser Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asn Val Glu Lys
390          530          535          540
392 gaa ctt aaa gcc cgt aag ctt aag tcc cgg ctc ctt ctt tcg gtg cac      1680
393 Glu Leu Lys Ala Arg Lys Leu Lys Ser Arg Leu Leu Leu Ser Val His
394 545          550          555          560
397 gat gag tta gtt tta gaa gtg ccg gcg gaa gag ctg gaa gag gta aaa      1728
398 Asp Glu Leu Val Leu Glu Val Pro Ala Glu Glu Leu Glu Glu Val Lys
399          565          570          575
401 gcg ctg gta aaa ggg gtt atg gag tcg gtg gtt gaa ctg aaa gtg cct      1776
402 Ala Leu Val Lys Gly Val Met Glu Ser Val Val Glu Leu Lys Val Pro
403          580          585          590
405 tta atc gct gaa gtt ggt gca ggc aaa aac tgg tat gaa gcg aag taa      1824
406 Leu Ile Ala Glu Val Gly Ala Gly Lys Asn Trp Tyr Glu Ala Lys
407          595          600          605
410 <210> SEQ ID NO: 11
412 <211> LENGTH: 607
414 <212> TYPE: PRT
416 <213> ORGANISM: Carboxydotherrmus hydrogenoformans
420 <400> SEQUENCE: 11
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423 1          5          10          15
426 Leu Ala Thr Ile Leu Arg Glu Ile Pro Leu Glu Ile Ser Leu Glu Asp
427          20          25          30
430 Leu Lys Val Lys Glu Pro Asn Tyr Glu Glu Val Ala Lys Leu Phe Leu
431          35          40          45
434 His Leu Glu Phe Lys Ser Phe Leu Lys Glu Ile Glu Pro Lys Ile Lys
435          50          55          60
438 Lys Glu Tyr Gln Glu Gly Lys Asp Leu Val Gln Val Glu Thr Val Glu
439 65          70          75          80
442 Thr Glu Gly Gln Ile Ala Val Val Phe Ser Asp Gly Phe Tyr Val Asp
443          85          90          95
446 Asp Gly Glu Lys Thr Lys Phe Tyr Ser Leu Asp Arg Leu Asn Glu Ile

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VERIFICATION SUMMARY

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L:23 M:270 C: Current Application Number differs, Replaced Current Application No
L:23 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:49 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:78 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:87 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:106 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:115 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:133 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:151 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:169 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:187 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:205 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:223 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:583 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12